



SEQ LIST US provisional App. No. 60051917

SEQUENCE LISTING

SEQ ID NO: 1
SEQUENCE LENGTH: 21
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
CTC TAG CAT GCG AAA ATC TAG

SEQ ID NO: 2
SEQUENCE LENGTH: 20
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
CTG CAG GCC TGC AAG CTT GG

SEQ ID NO: 3
SEQUENCE LENGTH: 23
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
ATC CTT TGT ATT TGA TTA AAG

SEQ ID NO: 4
SEQUENCE LENGTH: 20
SEQUENCE TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid
SEQUENCE DESCRIPTION:
TCT AGA GTC GAC CTG CAG GC

SEQ ID NO: 5
SEQUENCE LENGTH: 552
SEQUENCE TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*
SEQUENCE DESCRIPTION:
Met Glu Asn Met Glu Asn Asp Glu Asn Ile Val Val Gly Pro Lys
1 5 10 15
Pro Phe Tyr Pro Ile Glu Glu Gly Ser Ala Gly Thr Gln Leu Arg
20 25 30
Lys Tyr Met Glu Arg Tyr Ala Lys Leu Gly Ala Ile Ala Phe Thr
35 40 45
Asn Ala Val Thr Gly Val Asp Tyr Ser Tyr Ala Glu Tyr Leu Glu
50 55 60
Lys Ser Cys Cys Leu Gly Lys Ala Leu Gln Asn Tyr Gly Leu Val
65 70 75
Val Asp Gly Arg Ile Ala Leu Cys Ser Glu Asn Cys Glu Glu Phe

SEQ LIST US provisional App. No. 60051917

	80		85		90
Phe Ile Pro Val	Ile	Ala Gly Leu Phe	Ile Gly Val Gly Val	Ala	
	95		100		105
Pro Thr Asn Glu	Ile	Tyr Thr Leu Arg	Glu Leu Val His Ser	Leu	
	110		115		120
Gly Ile Ser Lys	Pro	Thr Ile Val Phe	Ser Ser Lys Lys Gly	Leu	
	125		130		135
Asp Lys Val Ile	Thr	Val Gln Lys Thr	Val Thr Thr Ile Lys	Thr	
	140		145		150
Ile Val Ile Leu	Asp	Ser Lys Val Asp	Tyr Arg Gly Tyr Gln	Cys	
	155		160		165
Leu Asp Thr Phe	Ile	Lys Arg Asn Thr	Pro Pro Gly Phe Gln	Ala	
	170		175		180
Ser Ser Phe Lys	Thr	Val Glu Val Asp	Arg Lys Glu Gln Val	Ala	
	185		190		195
Leu Ile Met Asn	Ser	Ser Gly Ser Thr	Gly Leu Pro Lys Gly	Val	
	200		205		210
Gln Leu Thr His	Glu	Asn Thr Val Thr	Arg Phe Ser His Ala	Arg	
	215		220		225
Asp Pro Ile Phe	Gly	Asn Gln Ile Ile	Pro Asp Thr Ala Ile	Leu	
	230		235		240
Ser Val Val Pro	Phe	His His Gly Phe	Gly Met Phe Thr Thr	Leu	
	245		250		255
Gly Tyr Leu Ile	Cys	Gly Phe Arg Val	Val Leu Met Tyr Arg	Phe	
	260		265		270
Glu Glu Glu Leu	Phe	Leu Arg Ser Leu	Gln Asp Tyr Lys Ile	Gln	
	275		280		285
Ser Ala Leu Leu	Val	Pro Thr Leu Phe	Ser Phe Phe Ala Lys	Ser	
	290		295		300
Thr Leu Ile Asp	Lys	Tyr Asp Leu Ser	Asn Leu His Glu Ile	Ala	
	305		310		315
Ser Gly Gly Ala	Pro	Leu Ser Lys Glu	Val Gly Glu Ala Val	Ala	
	320		325		330
Lys Arg Phe His	Leu	Pro Gly Ile Arg	Gln Gly Tyr Gly Leu	Thr	
	335		340		345
Glu Thr Thr Ser	Ala	Ile Leu Ile Thr	Pro Glu Gly Asp Asp	Lys	
	350		355		360
Pro Gly Ala Val	Gly	Lys Val Val Pro	Phe Phe Glu Ala Lys	Val	
	365		370		375
Val Asp Leu Asp	Thr	Gly Lys Thr Leu	Gly Val Asn Gln Arg	Gly	
	380		385		390
Glu Leu Cys Val	Arg	Gly Pro Met Ile	Met Ser Gly Tyr Val	Asn	
	395		400		405
Asn Pro Glu Ala	Thr	Asn Ala Leu Ile	Asp Lys Asp Gly Trp	Leu	
	410		415		420
His Ser Gly Asp	Ile	Ala Tyr Trp Asp	Glu Asp Glu His Phe	Phe	
	425		430		435
Ile Val Asp Arg	Leu	Lys Ser Leu Ile	Lys Tyr Lys Gly Tyr	Gln	
	440		445		450
Val Ala Pro Ala	Glu	Leu Glu Ser Ile	Leu Leu Gln His Pro	Asn	
	455		460		465
Ile Phe Asp Ala	Gly	Val Ala Gly Leu	Pro Asp Asp Asp Ala	Gly	
	470		475		480
Glu Leu Pro Ala	Ala	Val Val Val Leu	Glu His Gly Lys Thr	Met	
	485		490		495
Thr Glu Lys Glu	Ile	Val Asp Tyr Val	Ala Ser Gln Val Thr	Thr	

SEQ LIST US provisional App. No. 60051917

500	Ala Lys Lys Leu	Arg Gly Gly Val Val	505	Phe Val Asp Glu Val	510
515	Lys Gly Leu Thr	Gly Lys Leu Asp Ala	520	Arg Lys Ile Arg Glu	525
530	Leu Ile Lys Ala	Lys Lys Gly Gly Lys	535	Ser Lys Leu	540
545			550		552

SEQ ID NO: 6

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

ATG	GAA	AAC	ATG	GAA	AAC	GAT	GAA	AAT	ATT	GTA	GTT	GGA	CCT	AAA	CCG	48
TTT	TAC	CCT	ATC	GAA	GAG	GGA	TCT	GCT	GGA	ACA	CAA	TTA	CGC	AAA	TAC	96
ATG	GAG	CGA	TAT	GCA	AAA	CTT	GGC	GCA	ATT	GCT	TTT	ACA	AAT	GCA	GTT	144
ACT	GGT	GTT	GAT	TAT	TCT	TAC	GCC	GAA	TAC	TTG	GAG	AAA	TCA	TGT	TGT	192
CTA	GGA	AAA	GCT	TTG	CAA	AAT	TAT	GGT	TTG	GTT	GTT	GAT	GGC	AGA	ATT	240
GCG	TTA	TGC	AGT	GAA	AAC	TGT	GAA	GAA	TTT	TTT	ATT	CCT	GTA	ATA	GCC	288
GGA	CTG	TTT	ATA	GGT	GTA	GGT	GTT	GCA	CCC	ACT	AAT	GAG	ATT	TAC	ACT	366
TTA	CGT	GAA	CTG	GTT	CAC	AGT	TTA	GGT	ATC	TCT	AAA	CCA	ACA	ATT	GTA	384
TTT	AGT	TCT	AAA	AAA	GGC	TTA	GAT	AAA	GTT	ATA	ACA	GTA	CAG	AAA	ACA	432
GTA	ACT	ACT	ATT	AAA	ACC	ATT	GTT	ATA	CTA	GAT	AGC	AAA	GTT	GAT	TAT	480
CGA	GGA	TAT	CAA	TGT	CTG	GAC	ACC	TTT	ATA	AAA	AGA	AAC	ACT	CCA	CCA	528
GGT	TTT	CAA	GCA	TCC	AGT	TTT	AAA	ACT	GTG	GAA	GTT	GAC	CGT	AAA	GAA	576
CAA	GTT	GCT	CTT	ATA	ATG	AAC	TCT	TCG	GGT	TCT	ACC	GGT	TTG	CCA	AAA	624
GGC	GTA	CAA	CTT	ACT	CAC	GAA	AAT	ACA	GTC	ACT	AGA	TTT	TCG	CAT	GCC	672
AGA	GAT	CCT	ATT	TTT	GGC	AAT	CAA	ATC	ATT	CCG	GAT	ACT	GCG	ATT	TTA	720
AGT	GTT	GTT	CCA	TTC	CAT	CAC	GGT	TTT	GGA	ATG	TTT	ACT	ACA	CTC	GGA	768
TAT	TTG	ATA	TGT	GGA	TTT	CGA	GTC	GTC	TTA	ATG	TAT	AGA	TTT	GAA	GAA	816
GAG	CTG	TTT	TTA	CGA	TCC	CTT	CAG	GAT	TAC	AAA	ATT	CAA	AGT	GCG	TTG	864
CTA	GTA	CCA	ACC	CTA	TTT	TCA	TTC	TTC	GCC	AAA	AGC	ACT	CTG	ATT	GAC	912
AAA	TAC	GAT	TTA	TCT	AAT	TTA	CAC	GAA	ATT	GCT	TCT	GGG	GGC	GCA	CCT	960
CTT	TCG	AAA	GAA	GTC	GGG	GAA	GCG	GTT	GCA	AAA	CGC	TTC	CAT	CTT	CCA	1008
GGG	ATA	CGA	CAA	GGA	TAT	GGG	CTC	ACT	GAG	ACT	ACA	TCA	GCT	ATT	CTG	1056
ATT	ACA	CCC	GAG	GGG	GAT	GAT	AAA	CCG	GGC	GCG	GTC	GGT	AAA	GTT	GTT	1104
CCA	TTT	TTT	GAA	GCG	AAG	GTT	GTG	GAT	CTG	GAT	ACC	GGG	AAA	ACG	CTG	1152
GGC	GTT	AAT	CAG	AGA	GGC	GAA	TTA	TGT	GTC	AGA	GGA	CCT	ATG	ATT	ATG	1200
TCC	GGT	TAT	GTA	AAC	AAT	CCG	GAA	GCG	ACC	AAC	GCC	TTG	ATT	GAC	AAG	1248
GAT	GGA	TGG	CTA	CAT	TCT	GGA	GAC	ATA	GCT	TAC	TGG	GAC	GAA	GAC	GAA	1296
CAC	TTC	TTC	ATA	GTT	GAC	CGC	TTG	AAG	TCT	TTA	ATT	AAA	TAC	AAA	GGA	1344
TAT	CAG	GTG	GCC	CCC	GCT	GAA	TTG	GAA	TCG	ATA	TTG	TTA	CAA	CAC	CCC	1392
AAC	ATC	TTC	GAC	GCG	GGC	GTG	GCA	GGT	CTT	CCC	GAC	GAT	GAC	GCC	GGT	1440
GAA	CTT	CCC	GCC	GCC	GTT	GTT	GTT	TTG	GAG	CAC	GGA	AAG	ACG	ATG	ACG	1488
GAA	AAA	GAG	ATC	GTG	GAT	TAC	GTC	GCC	AGT	CAA	GTA	ACA	ACC	GCG	AAA	1536
AAG	TTG	CGC	GGA	GGA	GTT	GTG	TTT	GTG	GAC	GAA	GTA	CCG	AAA	GGT	CTT	1584
ACC	GGA	AAA	CTC	GAC	GCA	AGA	AAA	ATC	AGA	GAG	ATC	CTC	ATA	AAG	GCC	1632
AAG	AAG	GGC	GGA	AAG	TCC	AAA	TTG									1656

SEQ ID NO: 7

SEQUENCE LENGTH: 552

SEQUENCE TYPE: amino acid

TOPOLOGY: linear

SEQ LIST US provisional App. No. 60051917

MOLECULE TYPE: peptide

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

Met	Glu	Asn	Met	Glu	Asn	Asp	Glu	Asn	Ile	Val	Val	Gly	Pro	Lys	1	5	10	15
Pro	Phe	Tyr	Pro	Ile	Glu	Glu	Gly	Ser	Ala	Gly	Thr	Gln	Leu	Arg	20	25	30	35
Lys	Tyr	Met	Glu	Arg	Tyr	Ala	Lys	Leu	Gly	Ala	Ile	Ala	Phe	Thr	40	45	50	55
Asn	Ala	Val	Thr	Gly	Val	Asp	Tyr	Ser	Tyr	Ala	Glu	Tyr	Leu	Glu	60	65	70	75
Lys	Ser	Cys	Cys	Leu	Gly	Lys	Ala	Leu	Gln	Asn	Tyr	Gly	Leu	Val	80	85	90	95
Val	Asp	Gly	Arg	Ile	Ala	Leu	Cys	Ser	Glu	Asn	Cys	Glu	Glu	Phe	100	105	110	115
Phe	Ile	Pro	Val	Ile	Ala	Gly	Leu	Phe	Ile	Gly	Val	Gly	Val	Ala	120	125	130	135
Pro	Thr	Asn	Glu	Ile	Tyr	Thr	Leu	Arg	Glu	Leu	Val	His	Ser	Leu	140	145	150	155
Gly	Ile	Ser	Lys	Pro	Thr	Ile	Val	Phe	Ser	Ser	Lys	Lys	Gly	Leu	160	165	170	175
Asp	Lys	Val	Ile	Thr	Val	Gln	Lys	Thr	Val	Thr	Thr	Ile	Lys	Thr	180	185	190	195
Ile	Val	Ile	Leu	Asp	Ser	Lys	Val	Asp	Tyr	Arg	Gly	Tyr	Gln	Cys	200	205	210	215
Leu	Asp	Thr	Phe	Ile	Lys	Arg	Asn	Thr	Pro	Pro	Gly	Phe	Gln	Ala	220	225	230	235
Ser	Ser	Phe	Lys	Thr	Val	Glu	Val	Asp	Arg	Lys	Glu	Gln	Val	Ala	240	245	250	255
Leu	Ile	Met	Asn	Ser	Ser	Gly	Ser	Thr	Gly	Leu	Pro	Lys	Gly	Val	260	265	270	275
Gln	Leu	Thr	His	Glu	Asn	Ile	Val	Thr	Arg	Phe	Ser	His	Ala	Arg	280	285	290	295
Asp	Pro	Ile	Tyr	Gly	Asn	Gln	Val	Ser	Pro	Gly	Thr	Ala	Val	Leu	300	305	310	315
Thr	Val	Val	Pro	Phe	His	His	Gly	Phe	Gly	Met	Phe	Thr	Thr	Leu	320	325	330	335
Gly	Tyr	Leu	Ile	Cys	Gly	Phe	Arg	Val	Val	Met	Leu	Thr	Lys	Phe	340	345	350	355
Asp	Glu	Glu	Thr	Phe	Leu	Lys	Thr	Leu	Gln	Asp	Tyr	Lys	Cys	Thr	360	365	370	375
Ser	Val	Ile	Leu	Val	Pro	Thr	Leu	Phe	Ala	Ile	Leu	Asn	Lys	Ser	380	385	390	395
Glu	Leu	Leu	Asn	Lys	Tyr	Asp	Leu	Ser	Asn	Leu	Val	Glu	Ile	Ala	400	405	410	415
Ser	Gly	Gly	Ala	Pro	Leu	Ser	Lys	Glu	Val	Gly	Glu	Ala	Val	Ala	420	425	430	435
Arg	Arg	Phe	Asn	Leu	Pro	Gly	Val	Arg	Gln	Gly	Tyr	Gly	Leu	Thr	440	445	450	455
Glu	Thr	Thr	Ser	Ala	Ile	Ile	Ile	Thr	Pro	Glu	Gly	Asp	Asp	Lys	460	465	470	475
Pro	Gly	Ala	Ser	Gly	Lys	Val	Val	Pro	Leu	Phe	Lys	Ala	Lys	Val	480	485	490	495
Ile	Asp	Leu	Asp	Thr	Lys	Lys	Ser	Leu	Gly	Pro	Asn	Arg	Arg	Gly	500	505	510	515
Glu	Val	Cys	Val	Lys	Gly	Pro	Met	Leu	Met	Lys	Gly	Tyr	Val	Asn	520	525	530	535

SEQ LIST US provisional App. No. 60051917

395	Asn Pro Glu Ala Thr	400	Lys Glu Leu Ile Asp Glu Glu Gly Trp	405	Leu
410	His Thr Gly Asp Ile	415	Gly Tyr Tyr Asp Glu Glu Lys His Phe	420	Phe
425	Ile Val Asp Arg Leu	430	Lys Ser Leu Ile Lys Tyr Lys Gly Tyr	435	Gln
440	Val Ala Pro Ala Glu	445	Leu Glu Ser Ile Leu Leu Gln His Pro	450	Asn
455	Ile Phe Asp Ala Gly	460	Val Ala Gly Leu Pro Asp Asp Asp Ala	465	Gly
470	Glu Leu Pro Ala Ala	475	Val Val Val Leu Glu His Gly Lys Thr	480	Met
485	Thr Glu Lys Glu Ile	490	Val Asp Tyr Val Ala Ser Gln Val Thr	495	Thr
500	Ala Lys Lys Leu Arg	505	Gly Gly Val Val Phe Val Asp Glu Val	510	Pro
515	Lys Gly Leu Thr Gly	520	Lys Leu Asp Ala Arg Lys Ile Arg Glu	525	Ile
530	Leu Ile Lys Ala Lys	535	Lys Gly Gly Lys Ser Lys Leu	540	
545		550		552	

SEQ ID NO: 8

SEQUENCE LENGTH: 1656

SEQUENCE TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULE TYPE: cDNA to mRNA

ORIGINAL SOURCE: *Luciola cruciata* and *Photinus pyralis*

SEQUENCE DESCRIPTION:

ATG GAA AAC ATG GAA AAC GAT GAA AAT ATT GTA GTT GGA CCT AAA CCG	48
TTT TAC CCT ATC GAA GAG GGA TCT GCT GGA ACA CAA TTA CGC AAA TAC	96
ATG GAG CGA TAT GCA AAA CTT GGC GCA ATT GCT TTT ACA AAT GCA GTT	144
ACT GGT GTT GAT TAT TCT TAC GCC GAA TAC TTG GAG AAA TCA TGT TGT	192
CTA GGA AAA GCT TTG CAA AAT TAT GGT TTG GTT GTT GAT GGC AGA ATT	240
GCG TTA TGC AGT GAA AAC TGT GAA GAA TTT TTT ATT CCT GTA ATA GCC	288
GGA CTG TTT ATA GGT GTA GGT GTT GCA CCC ACT AAT GAG ATT TAC ACT	336
TTA CGT GAA CTG GTT CAC AGT TTA GGT ATC TCT AAA CCA ACA ATT GTA	384
TTT AGT TCT AAA AAA GGC TTA GAT AAA GTT ATA ACA GTA CAG AAA ACA	432
GTA ACT ACT ATT AAA ACC ATT GTT ATA CTA GAT AGC AAA GTT GAT TAT	480
CGA GGA TAT CAA TGT CTG GAC ACC TTT ATA AAA AGA AAC ACT CCA CCA	528
GGT TTT CAA GCA TCC AGT TTC AAA ACT GTG GAA GTT GAC CGT AAA GAA	576
CAA GTT GCT CTT ATA ATG AAC TCT TCG GGT TCT ACC GGT TTG CCA AAA	624
GGC GTA CAA CTT ACT CAC GAA AAT ATA GTC ACT AGA TTT TCT CAT GCT	672
AGA GAT CCG ATT TAT GGT AAC CAA GTT TCA CCA GGC ACC GCT GTT TTA	720
ACT GTC GTT CCA TTC CAT CAT GGT TTT GGT ATG TTC ACT ACT CTA GGG	768
TAT TTA ATT TGT GGT TTT CGT GTT GTA ATG TTA ACA AAA TTC GAT GAA	816
GAA ACA TTT TTA AAA ACT CTA CAA GAT TAT AAA TGT ACA AGT GTT ATT	864
CTT GTA CCG ACC TTG TTT GCA ATT CTC AAC AAA AGT GAA TTA CTC AAT	912
AAA TAC GAT TTG TCA AAT TTA GTT GAG ATT GCA TCT GGC GGA GCA CCT	960
TTA TCA AAA GAA GTT GGT GAA GCT GTT GCT AGA CGC TTT AAT CTT CCC	1008
GGT GTT CGT CAA GGT TAT GGT TTA ACA GAA ACA ACA TCT GCC ATT ATT	1056
ATT ACA CCG GAA GGT GAC GAT AAA CCA GGA GCT TCT GGA AAA GTC GTG	1104
CCG TTG TTT AAA GCA AAA GTT ATT GAT CTT GAT ACT AAA AAA TCT TTA	1152
GGT CCT AAC AGA CGT GGA GAA GTT TGT GTT AAA GGA CCT ATG CTT ATG	1200
AAA GGT TAT GTA AAT AAT CCA GAA GCA ACA AAA GAA CTT ATT GAC GAA	1248

SEQ LIST US provisional App. No. 60051917																
GAA	GGT	TGG	CTG	CAC	ACC	GGA	GAT	ATT	GGA	TAT	TAT	GAT	GAA	GAA	AAA	1296
CAT	TTC	TTT	ATT	GTC	GAT	CGT	TTG	AAG	TCT	TTA	ATC	AAA	TAC	AAA	GGA	1344
TAT	CAG	GTG	GCC	CCC	GCT	GAA	TTG	GAA	TCG	ATA	TTG	TTA	CAA	CAC	CCC	1392
AAC	ATC	TTC	GAC	GCG	GGC	GTG	GCA	GGT	CTT	CCC	GAC	GAT	GAC	GCC	GGT	1440
GAA	CTT	CCC	GCC	GCC	GTT	GTT	GTT	TTG	GAG	CAC	GGA	AAG	ACG	ATG	ACG	1488
GAA	AAA	GAG	ATC	GTG	GAT	TAC	GTC	GCC	AGT	CAA	GTA	ACA	ACC	GCG	AAA	1536
AAG	TTG	CGC	GGA	GGA	GTT	GTG	TTT	GTG	GAC	GAA	GTA	CCG	AAA	GGT	CTT	1584
ACC	GGA	AAA	CTC	GAC	GCA	AGA	AAA	ATC	AGA	GAG	ATC	CTC	ATA	AAG	GCC	1632
AAG	AAG	GGC	GGA	AAG	TCC	AAA	TTG									1656